Claims

What is claimed is:

1. A method for predicting the likelihood that a subject will develop collaterals, comprising assaying the expression level of at least three in genes in said subject. in a sample obtained from said mammal.

2. The method according to claim 1, wherein the likelihood of collateral development is predicted by the altered expression of at least three, at least five, at least ten, at least twenty genes, or at least twenty genes in said sample.

3. The method according to claim 1, wherein the likelihood of collateral development is predicted by increased expression of at least three, at least five, at least ten, at least twenty genes, or at least twenty genes in said sample.

4. The method according to claim 1, wherein the likelihood of collateral development is predicted by decreased expression of at least three, at least five, at least ten, at least twenty genes, or at least twenty genes in said sample.

5. The method according to claim 1 or claim 2, wherein said genes are selected from the genes listed in Table 1.

6. The method according to claim 3, wherein said genes are selected from the genes listed in Table 2.

7. The method according to claim 4, wherein said genes are selected from the genes listed in Table 2.

8. The method according to claim 1 wherein said sample comprises blood from said subject.

9. The method according to claim 1, wherein said altered expression level is at least two fold higher or lower than a reference level.

10. The method of any of claims 1-9 wherein the level of gene expression is determined by assaying the level of protein expression in a sample.

11. A method for predicting the likelihood that a subject will develop collaterals, comprising detecting the presence of at least three genetic variations in a sample from said patient, wherein said genetic variations are SNPs or altered DNA methylation patterns..

12. The method according to claim 11, wherein the likelihood of collateral development is predicted by the presence of genetic variations in at least three, at least five, at least ten, at least twenty genes, or at least twenty genes in said sample.

13. The method according to claim 11 or 12, wherein said genes are selected from the group consisting of the genes listed in Table 1.

14. The method according to claim 1 or claim 11 wherein the method of assay comprises using a genetic microarray or quantitative PCR..

15. The method according to claim 11 wherein the assay comprises a method to detect DNA methylation patterns.

16. The method according to claim 11 wherein the assay comprises a method to detect single nucleotide polymorphisms.

17. A kit for carrying out the assay according to claim 1 or claim 11, wherein said assay is to be carried out using a PCR and wherein said kit comprises a set of primers suitable for amplifying at least three, at least five, at least ten, or at least twenty DNA or RNA sequences corresponding to the genes in Table 1.

18. A kit for carrying out the assay according to claim 11 wherein said kit comprises a nucleic acid array capable of detecting single nucleotide polymorphisms in a plurality of the genes identified in Table 1.

19. A kit according to claim 18 wherein said array is capable of detecting single nucleotide polymorphisms, if present, in a majority of the genes identified in Table 1.

20. The method according to claim 1, wherein the expression level of said genes is determined by measuring the concentration of the proteins encoded by said genes.

21. The method according to claim 20, wherein said proteins are soluble proteins.

22. The method according to claim 21, wherein said sample is blood and/or lymph.

23. The method according to claim 20, wherein the level of protein expressions is determined by ELISA.

24. A method of promoting collateral formation in a subject, comprising administering to said subject a composition that decreases expression of at least one gene identified in Table 2 and/or that increases expression of at least one gene identified in Table 3.

25. The method according to claim 24, wherein said composition comprises an antisense oligonucleotide, an siRNA molecule, an RNAi molecule, an oligonucleotide that binds to mRNA to form a triplex, or a DNA molecule that is transcribed in said subject to produce an antisense oligonucleotide, an siRNA molecule, an RNAi, or an oligonucleotide that binds to mRNA to form a triplex.

26. The method according to claim 24, wherein said composition comprises an antibody or a soluble protein receptor that binds to a protein that inhibits collateral formation in said subject.

27. The method according to claim 26, wherein said composition comprises a human antibody or a human soluble protein receptor.

28. The method according to claim 24, wherein said composition comprises a protein that is administered to supplement the loss of a protein encoded by a gene identified in Table 3.